

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 11:26:24 ; Search time 479 Seconds
(without alignments)
7495.308 Million cell updates/sec

Title: US-09-935-757-1
Perfect score: 1330
Sequence: 1 accagtggagccgttgccat.....tcacctttcagcagacgccg 1330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description
	1	1330	100.0 1330	24	AAD35114	<i>Applicants</i> Corynebacterium gl
	2	1330	100.0 2086	24	AAD35115	" Corynebacterium gl
	3	1330	100.0 349980	22	AAH68527	<i>EP1108770</i> C glutamicum codin
	4	648	48.7 648	25	ACA00415	C. glutamicum deri
	5	639	48.0 639	22	AAH66206	C glutamicum codin
	6	247.8	18.6 771	24	ABT05614	Mycobacterium tube
	7	247.8	18.6 771	25	ABZ71111	Mycobacterium tube
	8	247.8	18.6 75216	24	ABX09141	Mycobacterium tube
	9	247.8	18.6 4403765	22	AAI99683	Mycobacterium tube
	10	247.8	18.6 4411529	22	AAI99682	Mycobacterium tube
	11	190	14.3 492	22	AAH66207	C glutamicum codin
	12	190	14.3 492	25	ACA00416	C. glutamicum deri
c	13	177	13.3 639	22	AAH66205	C glutamicum codin
c	14	177	13.3 639	25	ACA00413	C. glutamicum deri
c	15	162	12.2 162	25	ACA00414	C. glutamicum deri
	16	53.8	4.0 651	21	AAA39563	M. tuberculosis an
c	17	53.8	4.0 4403765	22	AAI99683	Mycobacterium tube
c	18	53.8	4.0 4411529	22	AAI99682	Mycobacterium tube
c	19	53.6	4.0 14615	23	AAS59577	Propionibacterium
	20	52.6	4.0 618	22	AAH65820	C glutamicum codin
	21	52.6	4.0 618	25	ACA00184	C. glutamicum deri
	22	52.6	4.0 1148	24	AAD33871	Corynebacterium gl
	23	52.6	4.0 349980	22	AAH68526	C glutamicum codin
	24	45.6	3.4 552	21	AAA38400	Pseudomonas sp. WF
	25	45.6	3.4 11279	21	AAA38389	Pseudomonas sp. WF
	26	42.2	3.2 1211	24	AAL42355	Corynebacterium gl
	27	42.2	3.2 309400	22	AAH68534	C glutamicum codin
	28	42	3.2 647	15	AAQ70249	P. aeruginosa algU
	29	42	3.2 647	15	AAQ70242	P. aeruginosa algU
	30	42	3.2 647	21	AAA51919	P. aeruginosa AlgU
	31	40.2	3.0 603	22	AAH68381	C glutamicum codin
	32	40.2	3.0 603	25	ACA01297	C. glutamicum deri
c	33	39.4	3.0 1020	23	ABL21875	Drosophila melanog
	34	39.4	3.0 3143	23	ABL21874	Drosophila melanog
	35	39	2.9 1105	19	AAV44589	Mycobacterium tube
	36	37.2	2.8 14041	22	AAH48024	Internal control B
	37	36.8	2.8 349980	24	ABQ81848	Bifidobacterium lo
	38	36.4	2.7 579	22	AAH65249	C glutamicum codin
	39	36.4	2.7 579	25	ACA01964	C. glutamicum deri
	40	36.4	2.7 1109	24	AAD33874	Corynebacterium gl
c	41	36.4	2.7 349980	22	AAH64966	C glutamicum codin
c	42	36	2.7 796	21	AAF12446	Aspergillus oryzae
	43	35.8	2.7 10732	21	AAA10594	Gene encoding a su
	44	35.6	2.7 822	24	ABZ14781	Arabidopsis thalia
	45	35.6	2.7 1376	21	AAC38218	Arabidopsis thalia

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 11:16:33 ; Search time 474 Seconds
(without alignments)
6279.453 Million cell updates/sec

Title: US-09-935-757-1
Perfect score: 1330
Sequence: 1 accagtggagccgttgccat.....tcacctttcagcagacgccg 1330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1504479 seqs, 1118970152 residues

Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 11:16:17 ; Search time 129 Seconds
(without alignments)
4550.694 Million cell updates/sec

Title: US-09-935-757-1
Perfect score: 1330
Sequence: 1 accagtggagccgttgccat.....tcacctttcagcagacgccg 1330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
	1	247.8	18.6	4403765	3	US-09-103-840A-2			Sequence 2, Appli
	2	247.8	18.6	4411529	3	US-09-103-840A-1			Sequence 1, Appli
	3	227.8	17.1	38675	4	US-08-311-731A-135			Sequence 135, App
c	4	53.8	4.0	4403765	3	US-09-103-840A-2			Sequence 2, Appli
c	5	53.8	4.0	4411529	3	US-09-103-840A-1			Sequence 1, Appli
	6	42	3.2	647	1	US-08-260-202A-9			Sequence 9, Appli
	7	42	3.2	647	1	US-08-017-114-9			Sequence 9, Appli
	8	42	3.2	647	3	US-08-505-307-9			Sequence 9, Appli
	9	42	3.2	647	4	US-09-609-151A-9			Sequence 9, Appli
	10	42	3.2	647	5	PCT-US94-02034-9			Sequence 9, Appli
	11	42	3.2	840	4	US-09-252-991A-13069			Sequence 13069, A